

SEQUENCE LISTING

<110> Tanzi, Rudolph E.  
Kovacs, Dora  
Saunders, Aleister J.

<120> Alpha-2-Macroglobulin Therapies and Drug Screening Methods for  
Alzheimer's Disease

<130> 0609.4460005

<140>  
<141>  
  
<150> 09/241,606  
<151> 1999-02-02  
  
<150> 09/148,503  
<151> 1998-09-04  
  
<150> 60/093,297  
<151> 1998-07-17  
  
<160> 27

<170> PatentIn Ver. 2.0

<210> 1  
<211> 4577  
<212> DNA  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> (44)..(112)

<220>  
<221> CDS  
<222> (44)..(4468)

<220>  
<221> mat\_peptide  
<222> (113)..(4468)

<400> 1  
gctacaatcc atctggtctc ctccagctcc ttctttctgc aac atg ggg aag aac 55  
Met Gly Lys Asn  
-20

aaa ctc ctt cat cca agt ctg gtt ctt ctc ctc ttg gtc ctc ctg ccc 103  
Lys Leu Leu His Pro Ser Leu Val Leu Leu Leu Val Leu Leu Pro  
-15 -10 -5

aca gac gcc tca gtc tct gga aaa ccg cag tat atg gtt ctg gtc ccc 151  
Thr Asp Ala Ser Val Ser Gly Lys Pro Gln Tyr Met Val Leu Val Pro  
-1 1 5 10

tcc ctg ctc cac act gag acc act gag aag ggc tgt gtc ctt ctg agc 199  
Ser Leu Leu His Thr Glu Thr Glu Lys Gly Cys Val Leu Leu Ser  
15 20 25

tac ctg aat gag aca gtg act gta agt gct tcc ttg gag tct gtc agg 247  
Tyr Leu Asn Glu Thr Val Thr Val Ser Ala Ser Leu Glu Ser Val Arg  
30 35 40 45

gga aac agg agc ctc ttc act gac ctg gag gcg gag aat gac gta ctc 295  
Gly Asn Arg Ser Leu Phe Thr Asp Leu Glu Ala Glu Asn Asp Val Leu  
50 55 60

cac tgt gtc gcc ttc gct gtc cca aag tct tca tcc aat gag gag gta 343  
His Cys Val Ala Phe Ala Val Pro Lys Ser Ser Asn Glu Glu Val  
65 70 75

atg ttc ctc act gtc caa gtg aaa gga cca acc caa gaa ttt aag aag 391  
Met Phe Leu Thr Val Gln Val Lys Gly Pro Thr Gln Glu Phe Lys Lys  
80 85 90

cgg acc aca gtg atg gtt aag aac gag gac agt ctg gtc ttt gtc cag 439  
Arg Thr Thr Val Met Val Lys Asn Glu Asp Ser Leu Val Phe Val Gln  
95 100 105

aca gac aaa tca atc tac aaa cca ggg cag aca gtg aaa ttt cgt gtt 487  
Thr Asp Lys Ser Ile Tyr Lys Pro Gly Gln Thr Val Lys Phe Arg Val  
110 115 120 125

gtc tcc atg gat gaa aac ttt cac ccc ctg aat gag ttg att cca cta 535  
Val Ser Met Asp Glu Asn Phe His Pro Leu Asn Glu Leu Ile Pro Leu  
130 135 140

gta tac att cag gat ccc aaa gga aat cgc atc gca caa tgg cag agt 583  
Val Tyr Ile Gln Asp Pro Lys Gly Asn Arg Ile Ala Gln Trp Gln Ser  
145 150 155

ttc cag tta gag ggt ggc ctc aag caa ttt tct ttt ccc ctc tca tca 631  
Phe Gln Leu Glu Gly Leu Lys Gln Phe Ser Phe Pro Leu Ser Ser  
160 165 170

gag ccc ttc cag ggc tcc tac aag gtg gtg gta cag aag aaa tca ggt 679  
Glu Pro Phe Gln Gly Ser Tyr Lys Val Val Gln Lys Lys Ser Gly  
175 180 185

gga agg aca gag cac cct ttc acc gtg gag gaa ttt gtt ctt ccc aag 727  
Gly Arg Thr Glu His Pro Phe Thr Val Glu Glu Phe Val Leu Pro Lys  
190 195 200 205

ttt gaa gta caa gta aca gtg cca aag ata atc acc atc ttg gaa gaa 775  
Phe Glu Val Gln Val Thr Val Pro Lys Ile Ile Thr Ile Leu Glu Glu  
210 215 220

gag atg aat gta tca gtg tgt ggc cta tac aca tat ggg aag cct gtc 823  
Glu Met Asn Val Ser Val Cys Gly Leu Tyr Thr Tyr Gly Lys Pro Val  
225 230 235

cct gga cat gtg act gtg agc att tgc aga aag tat agt gac gct tcc 871  
Pro Gly His Val Thr Val Ser Ile Cys Arg Lys Tyr Ser Asp Ala Ser  
240 245 250

gac tgc cac ggt gaa gat tca cag gct ttc tgt gag aaa ttc agt gga 919  
Asp Cys His Gly Glu Asp Ser Gln Ala Phe Cys Glu Lys Phe Ser Gly  
255 260 265

cag cta aac agc cat ggc tgc ttc tat cag caa gta aaa acc aag gtc 967  
Gln Leu Asn Ser His Gly Cys Phe Tyr Gln Gln Val Lys Thr Lys Val  
270 275 280 285

ttc cag ctg aag agg aag gag tat gaa atg aaa ctt cac act gag gcc 1015  
Phe Gln Leu Lys Arg Lys Glu Tyr Glu Met Lys Leu His Thr Glu Ala  
290 295 300

cag atc caa gaa gaa gga aca gtg gtg gaa ttg act gga agg cag tcc 1063  
Gln Ile Gln Glu Glu Gly Thr Val Val Glu Leu Thr Gly Arg Gln Ser  
305 310 315

agt gaa atc aca aga acc ata acc aaa ctc tca ttt gtg aaa gtg gac 1111  
Ser Glu Ile Thr Arg Thr Ile Thr Lys Leu Ser Phe Val Lys Val Asp  
320 325 330

tca cac ttt cga cag gga att ccc ttc ttt ggg cag gtg cgc cta gta 1159  
Ser His Phe Arg Gln Gly Ile Pro Phe Phe Gly Gln Val Arg Leu Val  
335 340 345

gat ggg aaa ggc gtc cct ata cca aat aaa gtc ata ttc atc aga gga 1207  
Asp Gly Lys Gly Val Pro Ile Pro Asn Lys Val Ile Phe Ile Arg Gly  
350 355 360 365

aat gaa gca aac tat tac tcc aat gct acc acg gat gag cat ggc ctt 1255  
Asn Glu Ala Asn Tyr Tyr Ser Asn Ala Thr Thr Asp Glu His Gly Leu  
370 375 380

gta cag ttc tct atc aac acc aac gtt atg ggt acc tct ctt act 1303  
Val Gln Phe Ser Ile Asn Thr Thr Asn Val Met Gly Thr Ser Leu Thr  
385 390 395

gtt agg gtc aat tac aag gat cgt agt ccc tgt tac ggc tac cag tgg 1351  
Val Arg Val Asn Tyr Lys Asp Arg Ser Pro Cys Tyr Gly Tyr Gln Trp  
400 405 410

gtg tca gaa gaa cac gaa gag gca cat cac act gct tat ctt gtg ttc 1399  
Val Ser Glu Glu His Glu Ala His His Thr Ala Tyr Leu Val Phe  
415 420 425

tcc cca agc aag agc ttt gtc cac ctt gag ccc atg tct cat gaa cta 1447  
Ser Pro Ser Lys Ser Phe Val His Leu Glu Pro Met Ser His Glu Leu  
430 435 440 445

ccc tgt ggc cat act cag aca gtc cag gca cat tat att ctg aat gga 1495

Pro Cys Gly His Thr Gln Thr Val Gln Ala His Tyr Ile Leu Asn Gly  
450 455 460

ggc acc ctg ctg ggg ctg aag aag ctc tcc ttt tat tat ctg ata atg 1543  
Gly Thr Leu Leu Gly Leu Lys Lys Leu Ser Phe Tyr Tyr Leu Ile Met  
465 470 475

gca aag gga ggc att gtc cga act ggg act cat gga ctg ctt gtg aag 1591  
Ala Lys Gly Gly Ile Val Arg Thr Gly Thr His Gly Leu Leu Val Lys  
480 485 490

cag gaa gac atg aag ggc cat ttt tcc atc tca atc cct gtg aag tca 1639  
Gln Glu Asp Met Lys Gly His Phe Ser Ile Ser Ile Pro Val Lys Ser  
495 500 505

gac att gct cct gtc gct cgg ttg ctc atc tat gct gtt tta cct acc 1687  
Asp Ile Ala Pro Val Ala Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr  
510 515 520 525

ggg gac gtg att ggg gat tct gca aaa tat gat gtt gaa aat tgt ctg 1735  
Gly Asp Val Ile Gly Asp Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu  
530 535 540

gcc aac aag gtg gat ttg agc ttc agc cca tca caa agt ctc cca gcc 1783  
Ala Asn Lys Val Asp Leu Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala  
545 550 555

tca cac gcc cac ctg cga gtc aca gcg gct cct cag tcc gtc tgc gcc 1831  
Ser His Ala His Leu Arg Val Thr Ala Ala Pro Gln Ser Val Cys Ala  
560 565 570

ctc cgt gtg gac caa agc gtg ctc atg aag cct gat gct gag 1879  
Leu Arg Ala Val Asp Gln Ser Val Leu Leu Met Lys Pro Asp Ala Glu  
575 580 585

ctc tcg gcg tcc tcg gtt tac aac ctg cta cca gaa aag gac ctc act 1927  
Leu Ser Ala Ser Ser Val Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr  
590 595 600 605

ggc ttc cct ggg cct ttg aat gac cag gac gat gaa gac tgc atc aat 1975  
Gly Phe Pro Gly Pro Leu Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn

610

615

620

cgt cat aat gtc tat att aat gga atc aca tat act cca gta tca agt 2023  
Arg His Asn Val Tyr Ile Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser  
625 630 635

aca aat gaa aag gat atg tac agc ttc cta gag gac atg ggc tta aag 2071  
Thr Asn Glu Lys Asp Met Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys  
640 645 650

gca ttc acc aac tca aag att cgt aaa ccc aaa atg tgt cca cag ctt 2119  
Ala Phe Thr Asn Ser Lys Ile Arg Lys Pro Lys Met Cys Pro Gln Leu  
655 660 665

caa cag tat gaa atg cat gga cct gaa ggt cta cgt gta ggt ttt tat 2167  
Gln Gln Tyr Glu Met His Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr  
670 675 680 685

gag tca gat gta atg gga aga ggc cat gca cgc ctg gtg cat gtt gaa 2215  
Glu Ser Asp Val Met Gly Arg Gly His Ala Arg Leu Val His Val Glu  
690 695 700

gag cct cac acg gag acc gta cga aag tac ttc cct gag aca tgg atc 2263  
Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile  
705 710 715

tgg gat ttg gtg gtg gta aac tca gca ggg gtg gct gag gta gga gta 2311  
Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala Glu Val Gly Val  
720 725 730

aca gtc cct gac acc atc acc gag tgg aag gca ggg gcc ttc tgc ctg 2359  
Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu  
735 740 745

tct gaa gat gct gga ctt ggt atc tct tcc act gcc tct ctc cga gcc 2407  
Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala  
750 755 760 765

ttc cag ccc ttc ttt gtg gag ctt aca atg cct tac tct gtg att cgt 2455  
Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr Ser Val Ile Arg  
770 775 780

gga gag gcc ttc aca ctc aag gcc acg gtc cta aac tac ctt ccc aaa 2503  
Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys  
785 790 795

tgc atc cgg gtc agt gtg cag ctg gaa gcc tct ccc gcc ttc ctt gct 2551  
Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala  
800 805 810

gtc cca gtg gag aag gaa caa gcg cct cac tgc atc tgt gca aac ggg 2599  
Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile Cys Ala Asn Gly  
815 820 825

cgg caa act gtg tcc tgg gca gta acc cca aag tca tta gga aat gtg 2647  
Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser Leu Gly Asn Val  
830 835 840 845

aat ttc act gtg agc gca gag gca cta gag tct caa gag ctg tgt ggg 2695  
Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln Glu Leu Cys Gly  
850 855 860

act gag gtg cct tca gtt cct gaa cac gga agg aaa gac aca gtc atc 2743  
Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys Asp Thr Val Ile  
865 870 875

aag cct ctg ttg gtt gaa cct gaa gga cta gag aag gaa aca aca ttc 2791  
Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys Glu Thr Thr Phe  
880 885 890

aac tcc cta ctt tgt cca tca ggt ggt gag gtt tct gaa gaa tta tcc 2839  
Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser Glu Glu Leu Ser  
895 900 905

ctg aaa ctg cca cca aat gtg gta gaa gaa tct gcc cga gct tct gtc 2887  
Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala Arg Ala Ser Val  
910 915 920 925

tca gtt ttg gga gac ata tta ggc tct gcc atg caa aac aca caa aat 2935  
Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln Asn Thr Gln Asn  
930 935 940

ctt ctc cag atg ccc tat ggc tgt gga gag cag aat atg gtc ctc ttt 2983  
Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Val Leu Phe  
945 950 955

gct cct aac atc tat gta ctg gat tat cta aat gaa aca cag cag ctt 3031  
Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu  
960 965 970

act cca gag atc aag tcc aag gcc att ggc tat ctc aac act ggt tac 3079  
Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr  
975 980 985

cag aga cag ttg aac tac aaa cac tat gat ggc tcc tac agc acc ttt 3127  
Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe  
990 995 1000 1005

ggg gag cga tat ggc agg aac cag ggc aac acc tgg ctc aca gcc ttt 3175  
Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe  
1010 1015 1020

gtt ctg aag act ttt gcc caa gct cga gcc tac atc ttc atc gat gaa 3223  
Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu  
1025 1030 1035

gca cac att acc caa gcc ctc ata tgg ctc tcc cag agg cag aag gac 3271  
Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp  
1040 1045 1050

aat ggc tgt ttc agg agc tct ggg tca ctg ctc aac aat gcc ata aag 3319  
Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys  
1055 1060 1065

gga gga gta gaa gat gaa gtg acc ctc tcc gcc tat atc acc atc gcc 3367  
Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr Ile Thr Ile Ala  
1070 1075 1080 1085

ctt ctg gag att cct ctc aca gtc act cac cct gtt gtc cgc aat gcc 3415  
Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val Val Arg Asn Ala  
1090 1095 1100

ctg ttt tgc ctg gag tca gcc tgg aag aca gca caa gaa ggg gac cat 3463

Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln Glu Gly Asp His  
1105 1110 1115

gac agc cat gta tat acc aaa gca ctg ctg gcc tat gct ttt gcc ctg 3511  
Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu  
1120 1125 1130

gca ggt aac cag gac aag agg aag gaa gta ctc aag tca ctt aat gag 3559  
Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys Ser Leu Asn Glu  
1135 1140 1145

gaa gct gtg aag aaa gac aac tct gtc cat tgg gag cgc cct cag aaa 3607  
Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu Arg Pro Gln Lys  
1150 1155 1160 1165

ccc aag gca cca gtg ggg cat ttt tac gaa ccc cag gct ccc tct gct 3655  
Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln Ala Pro Ser Ala  
1170 1175 1180

gag gtg gag atg aca tcc tat gtg ctc ctc gct tat ctc acg gcc cag 3703  
Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln  
1185 1190 1195

cca gcc cca acc tcg gag gac ctg acc tct gca acc aac atc gtg aag 3751  
Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys  
1200 1205 1210

tgg atc acg aag cag cag aat gcc cag ggc ggt ttc tcc tcc acc cag 3799  
Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Phe Ser Ser Thr Gln  
1215 1220 1225

gac aca gtg gtg gct ctc cat gct ctg tcc aaa tat gga gcc gcc aca 3847  
Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr  
1230 1235 1240 1245

ttt acc agg act ggg aag gct gca cag gtg act atc cag tct tca ggg 3895  
Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly  
1250 1255 1260

aca ttt tcc agc aaa ttc caa gtg gac aac aac aat cgc ctg tta ctg 3943  
Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Arg Leu Leu

1265	1270	1275	
cag cag gtc tca ttg cca gag ctg cct ggg gaa tac agc atg aaa gtg 3991			
Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val			
1280	1285	1290	
aca gga gaa gga tgt gtc tac ctc cag acc tcc ttg aaa tac aat att 4039			
Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile			
1295	1300	1305	
ctc cca gaa aag gaa gag ttc ccc ttt gct tta gga gtg cag act ctg 4087			
Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu			
1310	1315	1320	1325
cct caa act tgt gat gaa ccc aaa gcc cac acc agc ttc caa atc tcc 4135			
Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser			
1330	1335	1340	
cta agt gtc agt tac aca ggg agc cgc tct gcc tcc aac atg gcg atc 4183			
Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile			
1345	1350	1355	
gtt gat gtg aag atg gtc tct ggc ttc att ccc ctg aag cca aca gtg 4231			
Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val			
1360	1365	1370	
aaa atg ctt gaa aga tct aac cat gtg agc cgg aca gaa gtc agc agc 4279			
Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser			
1375	1380	1385	
aac cat gtc ttg att tac ctt gat aag gtg tca aat cag aca ctg agc 4327			
Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser			
1390	1395	1400	1405
ttg ttc ttc acg gtt ctg caa gat gtc cca gta aga gat ctc aaa cca 4375			
Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro			
1410	1415	1420	
gcc ata gtg aaa gtc tat gat tac tac gag acg gat gag ttt gca atc 4423			
Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile			
1425	1430	1435	

gct gag tac aat gct cct tgc agc aaa gat ctt gga aat gct tga 4468  
Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala  
1440 1445 1450

agaccacaag gctgaaaagt gctttgctgg agtcctgttc tctgagctcc acagaagaca 4528  
cgtgttttg tatcttaaa gacttgatga ataaacactt tttctggc 4577

<210> 2

<211> 1474

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Lys Asn Lys Leu Leu His Pro Ser Leu Val Leu Leu Leu  
1 5 10 15

Val Leu Leu Pro Thr Asp Ala Ser Val Ser Gly Lys Pro Gln Tyr Met  
20 25 30

Val Leu Val Pro Ser Leu Leu His Thr Glu Thr Thr Glu Lys Gly Cys  
35 40 45

Val Leu Leu Ser Tyr Leu Asn Glu Thr Val Thr Val Ser Ala Ser Leu  
50 55 60

Glu Ser Val Arg Gly Asn Arg Ser Leu Phe Thr Asp Leu Glu Ala Glu  
65 70 75 80

Asn Asp Val Leu His Cys Val Ala Phe Ala Val Pro Lys Ser Ser Ser  
85 90 95

Asn Glu Glu Val Met Phe Leu Thr Val Gln Val Lys Gly Pro Thr Gln  
100 105 110

Glu Phe Lys Lys Arg Thr Thr Val Met Val Lys Asn Glu Asp Ser Leu  
115 120 125

Val Phe Val Gln Thr Asp Lys Ser Ile Tyr Lys Pro Gly Gln Thr Val

130 135 140  
Lys Phe Arg Val Val Ser Met Asp Glu Asn Phe His Pro Leu Asn Glu  
145 150 155 160  
Leu Ile Pro Leu Val Tyr Ile Gln Asp Pro Lys Gly Asn Arg Ile Ala  
165 170 175  
Gln Trp Gln Ser Phe Gln Leu Glu Gly Gly Leu Lys Gln Phe Ser Phe  
180 185 190  
Pro Leu Ser Ser Glu Pro Phe Gln Gly Ser Tyr Lys Val Val Val Gln  
195 200 205  
Lys Lys Ser Gly Gly Arg Thr Glu His Pro Phe Thr Val Glu Glu Phe  
210 215 220  
Val Leu Pro Lys Phe Glu Val Gln Val Thr Val Pro Lys Ile Ile Thr  
225 230 235 240  
Ile Leu Glu Glu Glu Met Asn Val Ser Val Cys Gly Leu Tyr Thr Tyr  
245 250 255  
Gly Lys Pro Val Pro Gly His Val Thr Val Ser Ile Cys Arg Lys Tyr  
260 265 270  
Ser Asp Ala Ser Asp Cys His Gly Glu Asp Ser Gln Ala Phe Cys Glu  
275 280 285  
Lys Phe Ser Gly Gln Leu Asn Ser His Gly Cys Phe Tyr Gln Gln Val  
290 295 300  
Lys Thr Lys Val Phe Gln Leu Lys Arg Lys Glu Tyr Glu Met Lys Leu  
305 310 315 320  
His Thr Glu Ala Gln Ile Gln Glu Glu Gly Thr Val Val Glu Leu Thr  
325 330 335  
Gly Arg Gln Ser Ser Glu Ile Thr Arg Thr Ile Thr Lys Leu Ser Phe  
340 345 350

Val Lys Val Asp Ser His Phe Arg Gln Gly Ile Pro Phe Phe Gly Gln  
355 360 365

Val Arg Leu Val Asp Gly Lys Gly Val Pro Ile Pro Asn Lys Val Ile  
370 375 380

Phe Ile Arg Gly Asn Glu Ala Asn Tyr Tyr Ser Asn Ala Thr Thr Asp  
385 390 395 400

Glu His Gly Leu Val Gln Phe Ser Ile Asn Thr Thr Asn Val Met Gly  
405 410 415

Thr Ser Leu Thr Val Arg Val Asn Tyr Lys Asp Arg Ser Pro Cys Tyr  
420 425 430

Gly Tyr Gln Trp Val Ser Glu Glu His Glu Glu Ala His His Thr Ala  
435 440 445

Tyr Leu Val Phe Ser Pro Ser Lys Ser Phe Val His Leu Glu Pro Met  
450 455 460

Ser His Glu Leu Pro Cys Gly His Thr Gln Thr Val Gln Ala His Tyr  
465 470 475 480

Ile Leu Asn Gly Gly Thr Leu Leu Gly Leu Lys Lys Leu Ser Phe Tyr  
485 490 495

Tyr Leu Ile Met Ala Lys Gly Gly Ile Val Arg Thr Gly Thr His Gly  
500 505 510

Leu Leu Val Lys Gln Glu Asp Met Lys Gly His Phe Ser Ile Ser Ile  
515 520 525

Pro Val Lys Ser Asp Ile Ala Pro Val Ala Arg Leu Leu Ile Tyr Ala  
530 535 540

Val Leu Pro Thr Gly Asp Val Ile Gly Asp Ser Ala Lys Tyr Asp Val  
545 550 555 560

Glu Asn Cys Leu Ala Asn Lys Val Asp Leu Ser Phe Ser Pro Ser Gln  
565 570 575

Ser Leu Pro Ala Ser His Ala His Leu Arg Val Thr Ala Ala Pro Gln  
580 585 590

Ser Val Cys Ala Leu Arg Ala Val Asp Gln Ser Val Leu Leu Met Lys  
595 600 605

Pro Asp Ala Glu Leu Ser Ala Ser Ser Val Tyr Asn Leu Leu Pro Glu  
610 615 620

Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu Asn Asp Gln Asp Asp Glu  
625 630 635 640

Asp Cys Ile Asn Arg His Asn Val Tyr Ile Asn Gly Ile Thr Tyr Thr  
645 650 655

Pro Val Ser Ser Thr Asn Glu Lys Asp Met Tyr Ser Phe Leu Glu Asp  
660 665 670

Met Gly Leu Lys Ala Phe Thr Asn Ser Lys Ile Arg Lys Pro Lys Met  
675 680 685

Cys Pro Gln Leu Gln Gln Tyr Glu Met His Gly Pro Glu Gly Leu Arg  
690 695 700

Val Gly Phe Tyr Glu Ser Asp Val Met Gly Arg Gly His Ala Arg Leu  
705 710 715 720

Val His Val Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro  
725 730 735

Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala  
740 745 750

Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly  
755 760 765

Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala  
770 775 780

Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr

785 790 795 800  
Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn  
805 810 815  
Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro  
820 825 830  
Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile  
835 840 845  
Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser  
850 855 860  
Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln  
865 870 875 880  
Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys  
885 890 895  
Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys  
900 905 910  
Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser  
915 920 925  
Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala  
930 935 940  
Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln  
945 950 955 960  
Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn  
965 970 975  
Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu  
980 985 990  
Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr Leu  
995 1000 1005

Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser  
1010 1015 1020

Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp  
1025 1030 1035 1040

Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile  
1045 1050 1055

Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln  
1060 1065 1070

Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn  
1075 1080 1085

Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr  
1090 1095 1100

Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val  
1105 1110 1115 1120

Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln  
1125 1130 1135

Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr  
1140 1145 1150

Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys  
1155 1160 1165

Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu  
1170 1175 1180

Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln  
1185 1190 1195 1200

Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr  
1205 1210 1215

Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr  
1220 1225 1230

Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe  
1235 1240 1245

Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr  
1250 1255 1260

Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile  
1265 1270 1275 1280

Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn  
1285 1290 1295

Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr  
1300 1305 1310

Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu  
1315 1320 1325

Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly  
1330 1335 1340

Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser  
1345 1350 1355 1360

Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser  
1365 1370 1375

Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu  
1380 1385 1390

Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr  
1395 1400 1405

Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn  
1410 1415 1420

Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg  
1425 1430 1435 1440

Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp

1445

1450

1455

Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly  
1460 1465 1470

Asn Ala

<210> 3

<211> 750

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(750)

<223> A<sub>B</sub>/LRP Binding Domain

<400> 3

tcg gag gac ctg acc tct gca acc aac atc gtg aag tgg atc acg aag 48  
Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys  
1 5 10 15

cag cag aat gcc cag ggc ggt ttc tcc tcc acc cag gac aca gtg gtg 96  
Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val  
20 25 30

gct ctc cat gct ctg tcc aaa tat gga gcc gcc aca ttt acc agg act 144  
Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr  
35 40 45

ggg aag gct gca cag gtg act atc cag tct tca ggg aca ttt tcc agc 192  
Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser  
50 55 60

aaa ttc caa gtg gac aac aac aat cgc ctg tta ctg cag cag gtc tca 240  
Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Gln Gln Val Ser  
65 70 75 80

ttg cca gag ctg cct ggg gaa tac agc atg aaa gtg aca gga gaa gga 288  
Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly

	85	90	95	
tgt gtc tac ctc cag acc tcc ttg aaa tac aat att ctc cca gaa aag				336
Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys	100	105	110	
gaa gag ttc ccc ttt gct tta gga gtg cag act ctg cct caa act tgt				384
Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys	115	120	125	
gat gaa ccc aaa gcc cac acc agc ttc caa atc tcc cta agt gtc agt				432
Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser	130	135	140	
tac aca ggg agc cgc tct gcc tcc aac atg gcg atc gtt gat gtg aag				480
Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys	145	150	155	160
atg gtc tct ggc ttc att ccc ctg aag cca aca gtg aaa atg ctt gaa				528
Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu	165	170	175	
aga tct aac cat gtg agc cgg aca gaa gtc agc agc aac cat gtc ttg				576
Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu	180	185	190	
att tac ctt gat aag gtg tca aat cag aca ctg agc ttg ttc acg				624
Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr	195	200	205	
gtt ctg caa gat gtc cca gta aga gat ctc aaa cca gcc ata gtg aaa				672
Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys	210	215	220	
gtc tat gat tac tac gag acg gat gag ttt gca atc gct gag tac aat				720
Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn	225	230	235	240
gct cct tgc agc aaa gat ctt gga aat gct				750
Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala	245	250		

<210> 4

<211> 250

<212> PRT

<213> Homo sapiens

<400> 4

Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys  
1 5 10 15

Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val  
20 25 30

Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr  
35 40 45

Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser  
50 55 60

Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Gln Gln Val Ser  
65 70 75 80

Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly  
85 90 95

Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys  
100 105 110

Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys  
115 120 125

Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser  
130 135 140

Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys  
145 150 155 160

Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu  
165 170 175

Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu  
180 185 190

Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr  
195 200 205

Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys  
210 215 220

Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn  
225 230 235 240

Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala  
245 250

<210> 5

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(333)

<223> A $\beta$  Binding Domain

<400> 5

tcg gag gac ctg acc tot gca acc aac atc gtg aag tgg atc acg aag 48  
Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys  
1 5 10 15

cag cag aat gcc cag ggc ggt ttc tcc tcc acc cag gac aca gtg gtg 96  
Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val  
20 25 30

gct ctc cat gct ctg tcc aaa tat gga gcc gca ttt acc agg act 144  
Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr  
35 40 45

ggg aag gct gca cag gtg act atc cag tct tca ggg aca ttt tcc agc 192  
Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser

50	55	60	
aaa ttc caa gtg gac aac aac aat cgc ctg tta ctg cag cag gtc tca			240
Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser			
65	70	75	80
ttg cca gag ctg cct ggg gaa tac agc atg aaa gtg aca gga gaa gga			288
Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly			
85	90	95	
tgt gtc tac ctc cag acc tcc ttg aaa tac aat att ctc cca gaa			333
Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu			
100	105	110	
<210> 6			
<211> 111			
<212> PRT			
<213> Homo sapiens			
<400> 6			
Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys			
1	5	10	15
Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val			
20	25	30	
Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr			
35	40	45	
Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser			
50	55	60	
Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser			
65	70	75	80
Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly			
85	90	95	
Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu			
100	105	110	

<210> 7  
<211> 417  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(417)  
<223> LRP Binding Domain

<400> 7

aag	gaa	gag	ttc	ccc	ttt	gct	tta	gga	gtg	cag	act	ctg	cct	caa	act	48
Lys	Glu	Glu	Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	
1			5							10					15	

tgt gat gaa ccc aaa gcc cac acc agc ttc caa atc tcc cta agt gtc 96

Cys	Asp	Glu	Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	
20										25					30	

agt tac aca ggg agc cgc tct gcc tcc aac atg gcg atc gtt gat gtg 144

Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	
35										40					45	

aag atg gtc tct ggc ttc att ccc ctg aag cca aca gtg aaa atg ctt 192

Lys	Met	Val	Ser	Gly	Ile	Phe	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	
50										55					60	

gaa aga tct aac cat gtg agc cgg aca gaa gtc agc agc aac cat gtc 240

Glu	Arg	Ser	Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val		
65									70					75		80	

ttg att tac ctt gat aag gtg tca aat cag aca ctg agc ttg ttc ttc 288

Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	
85										90					95	

acg gtt ctg caa gat gtc cca gta aga gat ctc aaa cca gcc ata gtg 336

Thr	Val	Leu	Gln	Asp	Val	Pro	Val	Arg	Asp	Leu	Lys	Pro	Ala	Ile	Val	
100										105					110	

aaa gtc tat gat tac tac gag acg gat gag ttt gca atc gct gag tac 384  
Lys Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr  
115 120 125

aat gct cct tgc agc aaa gat ctt gga aat gct 417  
Asn Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala  
130 135

<210> 8  
<211> 139  
<212> PRT  
<213> Homo sapiens

<400> 8  
Lys Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr  
1 5 10 15

Cys Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val  
20 25 30

Ser Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val  
35 40 45

Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu  
50 55 60

Glu Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val  
65 70 75 80

Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe  
85 90 95

Thr Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val  
100 105 110

Lys Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr  
115 120 125

Asn Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala  
130 135

<210> 9  
<211> 81  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(81)  
<223> Consensus LRP Binding Domain

<400> 9  
ttc att ccc ctg aag cca aca gtg aaa atg ctt gaa aga tct aac cat 48  
Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His  
1 5 10 15  
  
gtg agc cgg aca gaa gtc agc agc aac cat gtc 81  
Val Ser Arg Thr Glu Val Ser Ser Asn His Val  
20 25

<210> 10  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 10  
Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His  
1 5 10 15  
  
Val Ser Arg Thr Glu Val Ser Ser Asn His Val  
20 25

<210> 11  
<211> 33  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(33)

<223> A $\beta$  Fibril Inhibitor

<400> 11

cgc gat ctg cca ttc ttc cca gtc cca att gat 33  
Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp  
1 5 10

<210> 12

<211> 11

<212> PRT

<213> Homo sapiens

<400> 12

Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp  
1 5 10

<210> 13

<211> 114

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(114)

<223> A $\beta$  Fibril Inhibitor

<400> 13

cgc gat ctg cca ttc ttc cca gtc cca att gat ttc att ccc ctg aag 48  
Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp Phe Ile Pro Leu Lys  
1 5 10 15

cca aca gtg aaa atg ctt gaa aga tct aac cat gtg agc cg<sup>g</sup> aca gaa 96  
Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr Glu  
20 25 30

gtc agc agc aac cat gtc 114  
Val Ser Ser Asn His Val

35

<210> 14  
<211> 38  
<212> PRT  
<213> Homo sapiens

<400> 14  
Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp Phe Ile Pro Leu Lys  
1 5 10 15  
Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr Glu  
20 25 30  
Val Ser Ser Asn His Val  
35

<210> 15  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(27)

<400> 15  
cgc gat ctg cca ttc ttc cca gtc gat 27  
Arg Asp Leu Pro Phe Phe Pro Val Asp  
1 5

<210> 16  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 16  
Arg Asp Leu Pro Phe Phe Pro Val Asp

1

5

<210> 17  
<211> 21  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(21)

<400> 17  
ctg cca ttc ttc cca gtc gat  
Leu Pro Phe Phe Pro Val Asp  
1 5

21

<210> 18  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 18  
Leu Pro Phe Phe Pro Val Asp  
1 5

<210> 19  
<211> 18  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(18)

<400> 19  
ctg cca ttc ttc gtc gat  
Leu Pro Phe Phe Val Asp  
1 5

18

<210> 20  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 20  
Leu Pro Phe Phe Val Asp  
1 5

<210> 21  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(15)

<400> 21  
ctg cca ttc ttc gat 15  
Leu Pro Phe Phe Asp  
1 5

<210> 22  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 22  
Leu Pro Phe Phe Asp  
1 5

<210> 23  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(12)

<400> 23  
ctg cca ttc ttc  
Leu Pro Phe Phe  
1

12

<210> 24  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 24  
Leu Pro Phe Phe  
1

<210> 25  
<211> 9  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(9)

<400> 25  
cca ttc ttc  
Pro Phe Phe  
1

9

<210> 26  
<211> 3  
<212> PRT  
<213> Homo sapiens

<400> 26

Pro Phe Phe  
1

<210> 27

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<223> Noncoding-antisense DNA

<400> 27

catgcaccag gcgtgcattgg cctcttccca ttacatctga ctctgagtga

50